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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 23:00:18 ; Search time 1096 Seconds
(without alignments)
557.627 Million cell updates/sec

Title: US-09-723-326B-1
Perfect score: 21
Sequence: 1 tgtcacgtcctgcacgacgta 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		21	100.0	21	6	AX189770	AX189770 Sequence
2		21	100.0	43	6	AX189774	AX189774 Sequence
3		21	100.0	86	6	AX189775	AX189775 Sequence
4		21	100.0	129	6	AX189778	AX189778 Sequence
5	c	20	95.2	24	6	AX147416	AX147416 Sequence
6	c	19	90.5	19	6	AX147421	AX147421 Sequence
7	c	19	90.5	24	6	A46287	A46287 Sequence 2
8	c	19	90.5	24	6	AX023673	AX023673 Sequence
9	c	19	90.5	24	6	AX048713	AX048713 Sequence
10		19	90.5	24	6	AX147415	AX147415 Sequence
11	c	19	90.5	41	6	AR073928	AR073928 Sequence
12		19	90.5	123	6	AX189776	AX189776 Sequence
13	c	19	90.5	229	6	AX023662	AX023662 Sequence
14	c	19	90.5	366	5	AF353996	AF353996 Cyprinus
15	c	19	90.5	513	6	AX150246	AX150246 Sequence
16	c	19	90.5	1110	10	MUSPGK1	M18735 Mouse phosp
17	c	19	90.5	1943	10	MMPGK5R	X15339 M.musculus
18	c	19	90.5	3297	12	AF090453	AF090453 Cloning v
19	c	19	90.5	3426	12	AF090454	AF090454 Cloning v
20	c	19	90.5	4699	12	AF346623	AF346623 RAGE vect
21	c	19	90.5	4768	6	AX299821	AX299821 Sequence
22	c	19	90.5	4768	6	AX352704	AX352704 Sequence
23	c	19	90.5	4847	6	AX191674	AX191674 Sequence
24	c	19	90.5	5365	6	AX114854	AX114854 Sequence
25	c	19	90.5	5482	12	AF090455	AF090455 Cloning v
26	c	19	90.5	5505	2	AL831717	AL831717 Mus muscu
27	c	19	90.5	5568	12	AF335419	AF335419 Cloning v
28		19	90.5	5568	12	AF335420	AF335420 Cloning v
29		19	90.5	5608	12	AF092169	AF092169 Cloning v
30		19	90.5	5608	12	AF092172	AF092172 Cloning v
31		19	90.5	5608	12	AF092173	AF092173 Cloning v
32		19	90.5	5608	12	AF092174	AF092174 Cloning v
33		19	90.5	5608	12	AF092541	AF092541 Cloning v
34		19	90.5	5608	12	AF092542	AF092542 Cloning v
35		19	90.5	5608	12	AF092543	AF092543 Cloning v
36		19	90.5	5608	12	AF092567	AF092567 Cloning v
37		19	90.5	5830	12	AY028413	AY028413 YTT vecto
38	c	19	90.5	5842	12	AY028415	AY028415 YTT vecto
39		19	90.5	6293	12	AF397196	AF397196 Retrofitt
40	c	19	90.5	6355	6	AX299822	AX299822 Sequence
41	c	19	90.5	6355	6	AX352705	AX352705 Sequence
42	c	19	90.5	7090	6	AX150263	AX150263 Sequence
43		19	90.5	8157	2	AL831743	AL831743 Mus muscu
44	c	19	90.5	8387	6	AR070490	AR070490 Sequence
45	c	19	90.5	8388	6	AR179512	AR179512 Sequence

ALIGNMENTS

RESULT 1
AX189770
LOCUS AX189770 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from Patent WO0148187.
ACCESSION AX189770
VERSION AX189770.1 GI:15143141
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Webster,K.A.
TITLE A molecular switch for regulating mammalian gene expression
JOURNAL Patent: WO 0148187-A 1 05-JUL-2001;
The University of Miami (US)

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FEATURES             Location/Qualifiers
     source          1. .21
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                     /note="oligonucleotide"
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ORIGIN

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Qy          1 TGTCACGTCCTGCACGACGTA 21
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Db          1 TGTCACGTCCTGCACGACGTA 21


RESULT 2
AX189774
LOCUS       AX189774                43 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 5 from Patent WO0148187.
ACCESSION   AX189774
VERSION     AX189774.1  GI:15143145
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Webster,K.A.
  TITLE     A molecular switch for regulating mammalian gene expression
  JOURNAL   Patent: WO 0148187-A 5 05-JUL-2001;
            The University of Miami (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
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ORIGIN

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACGTA 21
              |||||||||||||||||||||
Db         23 TGTCACGTCCTGCACGACGTA 43


RESULT 3
AX189775
LOCUS       AX189775                86 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from Patent WO0148187.
ACCESSION   AX189775
VERSION     AX189775.1  GI:15143146
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Webster,K.A.
  TITLE     A molecular switch for regulating mammalian gene expression
  JOURNAL   Patent: WO 0148187-A 6 05-JUL-2001;
            The University of Miami (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT       16 a     32 c     22 g     16 t
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Qy          1 TGTCACGTCCTGCACGACGTA 21
              |||||||||||||||||||||
Db         23 TGTCACGTCCTGCACGACGTA 43


RESULT 4
AX189778
LOCUS       AX189778                129 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from Patent WO0148187.
ACCESSION   AX189778
VERSION     AX189778.1  GI:15143149
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 129)
  AUTHORS   Webster,K.A.
  TITLE     A molecular switch for regulating mammalian gene expression
  JOURNAL   Patent: WO 0148187-A 9 05-JUL-2001;
            The University of Miami (US)
FEATURES             Location/Qualifiers
     source          1. .129
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                     /note="oligonucleotide"
BASE COUNT       24 a     48 c     27 g     30 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACGTA 21
              |||||||||||||||||||||
Db         23 TGTCACGTCCTGCACGACGTA 43


RESULT 5
AX147416/c
LOCUS       AX147416                24 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 4 from Patent WO0136616.
ACCESSION   AX147416
VERSION     AX147416.1  GI:14346573
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Beuzard,Y., Payen,E., Scherman,D. and Bettan,M.
  TITLE     Acid nucleic construct bearing a system regulating the expression
            of a gene
  JOURNAL   Patent: WO 0136616-A 4 25-MAY-2001;
            INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
            (FR) ; Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="HRE2"
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Qy          1 TGTCACGTCCTGCACGACGT 20
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Db         23 TGTCACGTCCTGCACGACGT 4
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RESULT 6
AX147421/c
LOCUS       AX147421                19 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 9 from Patent WO0136616.
ACCESSION   AX147421
VERSION     AX147421.1  GI:14346578
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Beuzard,Y., Payen,E., Scherman,D. and Bettan,M.
  TITLE     Acid nucleic construct bearing a system regulating the expression
            of a gene
  JOURNAL   Patent: WO 0136616-A 9 25-MAY-2001;
            INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
            (FR) ; Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="HRE"
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||||
Db         19 TGTCACGTCCTGCACGACG 1


RESULT 7
A46287/c
LOCUS       A46287                  24 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 2 from Patent WO9521927.
ACCESSION   A46287
VERSION     A46287.1  GI:2300513
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Ratcliffe,P.J., Firth,J.D., Harris,A.L. and Pugh,C.W.
  TITLE     TARGETING GENE THERAPY
  JOURNAL   Patent: WO 9521927-A 2 17-AUG-1995;
            ISIS INNOVATION (GB)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||||
Db         21 TGTCACGTCCTGCACGACG 3


RESULT 8
AX023673/c
LOCUS       AX023673                24 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 15 from Patent WO0017371.
ACCESSION   AX023673
VERSION     AX023673.1  GI:10184034
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Binley,K.M. and Naylor,S.
  TITLE     Polynucleotide constructs and uses thereof
  JOURNAL   Patent: WO 0017371-A 15 30-MAR-2000;
            BINLEY KATIE MARY (GB) ; NAYLOR STUART (GB) ; OXFORD BIOMEDICA LTD
            (GB)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus sp."
                     /db_xref="taxon:10095"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN

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Qy          1 TGTCACGTCCTGCACGACG 19
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Db         21 TGTCACGTCCTGCACGACG 3


RESULT 9
AX048713/c
LOCUS       AX048713                24 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 13 from Patent WO0069908.
ACCESSION   AX048713
VERSION     AX048713.1  GI:12225858
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Ratcliffe,P.J., Maxwell,P.H. and Pugh,C.W.
  TITLE     Interaction between the vhl tumour suppressor and hypoxia inducible
            factor, and assay methods relating thereto
  JOURNAL   Patent: WO 0069908-A 13 23-NOV-2000;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10095"
BASE COUNT        6 a      6 c      8 g      4 t
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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||||
Db         21 TGTCACGTCCTGCACGACG 3


RESULT 10
AX147415
LOCUS       AX147415                24 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 3 from Patent WO0136616.
ACCESSION   AX147415
VERSION     AX147415.1  GI:14346572
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Beuzard,Y., Payen,E., Scherman,D. and Bettan,M.
  TITLE     Acid nucleic construct bearing a system regulating the expression
            of a gene
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  JOURNAL   Patent: WO 0136616-A 3 25-MAY-2001;
            INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
            (FR) ; Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .24
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                     /note="HRE1"
BASE COUNT        4 a      8 c      7 g      5 t
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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
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Db          6 TGTCACGTCCTGCACGACG 24


RESULT 11
AR073928/c
LOCUS       AR073928                  41 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 2 from patent US 5952226.
ACCESSION   AR073928
VERSION     AR073928.1  GI:10000688
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Aebischer,P., Deglon,N., Regulier,E. and Rinsch,C.
  TITLE     Hypoxia responsive EPO producing cells
  JOURNAL   Patent: US 5952226-A 2 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="unknown"
BASE COUNT        8 a     11 c     15 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||||
Db         41 TGTCACGTCCTGCACGACG 23


RESULT 12
AX189776
LOCUS       AX189776                  123 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from Patent WO0148187.
ACCESSION   AX189776
VERSION     AX189776.1  GI:15143147
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 123)
  AUTHORS   Webster,K.A.
  TITLE     A molecular switch for regulating mammalian gene expression
  JOURNAL   Patent: WO 0148187-A 7 05-JUL-2001;
            The University of Miami (US)
FEATURES             Location/Qualifiers
     source          1. .123
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BASE COUNT       22 a     47 c     32 g     22 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||||
Db        101 TGTCACGTCCTGCACGACG 119


RESULT 13
AX023662/c
LOCUS       AX023662                  229 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 4 from Patent WO0017371.
ACCESSION   AX023662
VERSION     AX023662.1  GI:10184023
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Binley,K.M. and Naylor,S.
  TITLE     Polynucleotide constructs and uses thereof
  JOURNAL   Patent: WO 0017371-A 4 30-MAR-2000;
            BINLEY KATIE MARY (GB) ; NAYLOR STUART (GB) ; OXFORD BIOMEDICA LTD
            (GB)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
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Db         30 TGTCACGTCCTGCACGACG 12


RESULT 14
AF353996/c
LOCUS       AF353996                  366 bp    DNA     linear   VRT 08-MAY-2001
DEFINITION  Cyprinus carpio pMThGH-transgene flanking sequence.
ACCESSION   AF353996
VERSION     AF353996.1  GI:13991589
KEYWORDS    .
SOURCE      Cyprinus carpio.
  ORGANISM  Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Wu,B., Sun,Y., Wang,Y. and Zhu,Z.
  TITLE     Molecular polymorphic and sequences flanking pMThGH-transgene in F4
            transgenic common carp
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 366)
  AUTHORS   Wu,B., Sun,Y., Wang,Y. and Zhu,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2001) Fish Genetics & Breeding, Institute of
            Hydrobiology, Academia Sinica, Luojiashan, Wuhan, Hubei 430072,
            P.R.China
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Cyprinus carpio"
                     /db_xref="taxon:7962"
     misc_feature    1. .366
                     /note="pMThGH-transgene flanking sequence; similar to Mus
                     musculus phosphoglycerate kinase-1 gene exon 1"
BASE COUNT       64 a    120 c    106 g     76 t
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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
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Db        236 TGTCACGTCCTGCACGACG 218


RESULT 15
AX150246/c
LOCUS       AX150246                513 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 1 from Patent WO0136615.
ACCESSION   AX150246
VERSION     AX150246.1  GI:14348266
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 513)
  AUTHORS   Kochanek,S. and Schiedner,G.
  TITLE     Permanent amniocyte cell line, the production thereof and its use
            for producing gene transfer vectors
  JOURNAL   Patent: WO 0136615-A 1 25-MAY-2001;
            Kochanek, Stefan (DE)
FEATURES             Location/Qualifiers
     source          1. .513
                     /organism="Mus sp."
                     /db_xref="taxon:10095"
                     /note="Phosphoglycerat-Kinase-Promoter"
BASE COUNT       79 a    171 c    161 g    102 t
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 513;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACG 19
              |||||||||||||||||||
Db        235 TGTCACGTCCTGCACGACG 217


Search completed: July  9, 2003, 12:38:35
Job time : 1098 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:41 ; Search time 145 Seconds
(without alignments)
326.151 Million cell updates/sec

Title: US-09-723-326B-1
Perfect score: 21
Sequence: 1 tgtcacgtcctgcacgacgta 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	22	AAH42134	HRE element from t
	2	21	100.0	43	22	AAH42138	Synapsin gene SIL
	3	21	100.0	86	22	AAH42139	Synapsin gene SIL
	4	21	100.0	129	22	AAH42142	Synapsin gene SIL
c	5	19	90.5	19	22	AAF85326	Nucleotide fragmen
c	6	19	90.5	24	16	AAQ99458	Hypoxia-inducible
c	7	19	90.5	24	20	AAZ11422	Hypoxia responsive
c	8	19	90.5	24	21	AAA12007	Murine HRE mPGK DN
c	9	19	90.5	24	22	AAC88980	Murine hypoxic res
	10	19	90.5	123	22	AAH42140	Synapsin gene SIL
c	11	19	90.5	229	20	AAZ11398	PGK derived enhanc
c	12	19	90.5	229	21	AAA11996	Murine PGK HRE der
c	13	19	90.5	513	22	AAH20729	Murine phosphoglyc
c	14	19	90.5	4768	22	AAS05243	Plasmid vector pDG
c	15	19	90.5	4768	24	ABL42019	Nucleotide sequenc
c	16	19	90.5	4768	24	AAD28659	Plasmid pDG2 vecto
c	17	19	90.5	4768	24	AAS17143	Gene targetting ve
c	18	19	90.5	4847	22	AAD09280	pGK-cre-pA vector
c	19	19	90.5	5365	22	AAD04928	Retroviral vector
c	20	19	90.5	5377	21	AAA53872	Expression vector
c	21	19	90.5	5581	22	AAH41035	Hprt gene containi
c	22	19	90.5	6355	22	AAS05244	Plasmid vector pDG
c	23	19	90.5	6355	24	ABL42020	Nucleotide sequenc
c	24	19	90.5	6355	24	AAD28660	Plasmid pDG4 vecto
c	25	19	90.5	6355	24	AAS17144	Gene targetting ve
c	26	19	90.5	7090	22	AAH20746	Plasmid STK146 DNA
	27	19	90.5	7617	18	AAV14354	Plasmid pGen-PGKgf
c	28	19	90.5	8388	15	AAQ78191	Vector M48 used fo
c	29	19	90.5	9725	21	AAA53873	Expression vector
c	30	19	90.5	9732	21	AAA53879	Expression vector
c	31	19	90.5	9738	21	AAA53874	Expression vector
c	32	19	90.5	9873	21	AAA53875	Expression vector
c	33	19	90.5	10054	21	AAA53876	Expression vector
c	34	19	90.5	11162	24	AAK99658	DNA of the gene ve
c	35	19	90.5	11162	24	ABA99937	Human TNK-TPA DNA.
c	36	19	90.5	11162	24	ABL55839	Human mutant tissu
c	37	19	90.5	11162	24	ABL54504	Gene vector sequen
c	38	19	90.5	13928	22	AAH77500	Haemophilia B gene
c	39	19	90.5	15692	20	AAX24731	London-FAD APP tar
c	40	19	90.5	15692	20	AAX24732	Swedish/London-FAD
	41	19	90.5	15701	20	AAX24733	Swedish-FAD APP713
c	42	18	85.7	18	16	AAQ99459	Hypoxia-inducible
c	43	18	85.7	18	21	AAA12053	Murine PGK1 derive
	44	18	85.7	72	20	AAZ11440	HRE-containing enh
	45	18	85.7	72	21	AAA12023	Murine PGK HRE HIF

ALIGNMENTS

RESULT 1
AAH42134
ID AAH42134 standard; DNA; 21 BP.
XX
AC AAH42134;
XX
DT 17-SEP-2001 (first entry)
XX
DE HRE element from the human phosphoroglycerate kinase gene.
XX
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalessemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma;
KW hypoxia response enhancer; HRE; phosphoroglycerate kinase gene; ss.
XX
OS Homo sapiens.
XX
PN WO200148187-A2.
XX
PD 05-JUL-2001.
XX
PF 15-DEC-2000; 2000WO-US33269.
XX
PR 23-DEC-1999; 99US-0171597.
PR 28-NOV-2000; 2000US-0723326.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Webster KA;
XX

DR WPI; 2001-441715/47.
XX
PT Novel isolated expression vector useful therapeutically, comprisessa
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 24; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalessemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents an oligonucleotide containing
CC the hypoxia response enhancer (HRE) element from the human
CC phosphoroglycerate kinase gene in the sense orientation. It is used
CC to produce vectors of the invention.
XX
SQ Sequence 21 BP; 4 A; 7 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||||||||||||||
Db 1 TGTCACGTCCTGCACGACGTA 21

RESULT 2
AAH42138
ID AAH42138 standard; DNA; 43 BP.
XX
AC AAH42138;
XX
DT 17-SEP-2001 (first entry)
XX
DE Synapsin gene SIL element and phosphoroglycerate kinase gene HRE element.
XX
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalessemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoroglycerate kinase gene; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200148187-A2.
XX
PD 05-JUL-2001.
XX
PF 15-DEC-2000; 2000WO-US33269.
XX
PR 23-DEC-1999; 99US-0171597.
PR 28-NOV-2000; 2000US-0723326.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Webster KA;
XX
DR WPI; 2001-441715/47.
XX
PT Novel isolated expression vector useful therapeutically, comprisessa
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 25; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalessemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoroglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
SQ Sequence 43 BP; 8 A; 16 C; 11 G; 8 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||||||||||||||
Db 23 TGTCACGTCCTGCACGACGTA 43

RESULT 3
AAH42139
ID AAH42139 standard; DNA; 86 BP.
XX
AC AAH42139;
XX
DT 17-SEP-2001 (first entry)
XX
DE Synapsin gene SIL element and phosphoroglycerate kinase gene HRE element.
XX
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalessemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoroglycerate kinase gene; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200148187-A2.
XX
PD 05-JUL-2001.
XX
PF 15-DEC-2000; 2000WO-US33269.

XX
PR 23-DEC-1999; 99US-0171597.
PR 28-NOV-2000; 2000US-0723326.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Webster KA;
XX
DR WPI; 2001-441715/47.
XX
PT Novel isolated expression vector useful therapeutically, comprisessa
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 25; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalessemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoroglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
SQ Sequence 86 BP; 16 A; 32 C; 22 G; 16 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||||||||||||||
Db 23 TGTCACGTCCTGCACGACGTA 43

RESULT 4
AAH42142
ID AAH42142 standard; DNA; 129 BP.
XX
AC AAH42142;
XX
DT 17-SEP-2001 (first entry)
XX
DE Synapsin gene SIL element and phosphoroglycerate kinase gene HRE element.
XX
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalessemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoroglycerate kinase gene; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200148187-A2.
XX
PD 05-JUL-2001.
XX
PF 15-DEC-2000; 2000WO-US33269.
XX
PR 23-DEC-1999; 99US-0171597.
PR 28-NOV-2000; 2000US-0723326.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Webster KA;
XX
DR WPI; 2001-441715/47.
XX
PT Novel isolated expression vector useful therapeutically, comprisessa
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 25; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalessemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoroglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
SQ Sequence 129 BP; 24 A; 48 C; 27 G; 30 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||||||||||||||
Db 23 TGTCACGTCCTGCACGACGTA 43

RESULT 5
AAF85326/c
ID AAF85326 standard; DNA; 19 BP.
XX
AC AAF85326;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide fragment of plasmid pBS-HRE10.
XX
KW Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
KW anemia; cancer; ischemia; erythropoietin; immunotherapy;
KW autoimmune disease; hH104; tTAk; ds.
XX
OS Synthetic.
XX
PN WO200136616-A2.
XX

PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-FR03207.
XX
PR 18-NOV-1999; 99FR-0014513.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (AVET) AVENTIS PHARMA SA.
XX
PI Beuzard Y, Payen E, Scherman D, Bettan M;
XX
DR WPI; 2001-343818/36.
XX
PT New nucleic acid construct for controlling expression of target gene,
PT useful e.g. for treating cancer, is modulated by exogeneous
PT pharmaceutical and oxygen partial pressure -
XX
PS Disclosure; Page 18; 60pp; French.
XX
CC The specification describes a nucleic acid construct bearing a system
CC for regulating the expression of a gene. The nucleic acid construct
CC comprises at least one sequence encoding a protein that regulates
CC expression of at least one gene of interest. The activity of this
CC protein is modulated by presence/absence of a pharmacological agent
CC and the amount of protein produced depends on the oxygen partial
CC pressure. The constructs are used to treat conditions associated with
CC cellular hypoxia, especially anemia, cancer and ischemia, specifically
CC where the gene of interest encodes erythropoietin (but many other
CC suitable genes are listed, e.g. those encoding single-chain antibodies
CC for immunotherapy of infections or autoimmune diseases,
CC prodrug-converting enzymes, apoptosis inducers etc.). The present
CC sequence represents a fragment of pBS-HRE10, which was used to produce
CC constructs of the invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;

Query Match 90.5%; Score 19; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 19 TGTCACGTCCTGCACGACG 1

RESULT 6
AAQ99458/c
ID AAQ99458 standard; DNA; 24 BP.
XX
AC AAQ99458;
XX
DT 19-MAR-1996 (first entry)
XX
DE Hypoxia-inducible phosphoglycerate kinase-1 expression control sequence.
XX
KW Hypoxia; response element; erythropoietin; phosphoglycerate kinase;
KW PGK-1; gene therapy; tumour; cancer; P18; P24; ss.
XX
OS Mus sp.
XX
PN WO9521927-A2.
XX
PD 17-AUG-1995.
XX
PF 15-FEB-1995; 95WO-GB00322.
XX
PR 15-FEB-1994; 94GB-0002857.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Firth JD, Harris AL, Pugh CW, Ratcliffe PJ;
XX
DR WPI; 1995-293128/38.
XX
PT Novel method of targetting gene therapy - using a hypoxically
PT inducible expression control sequence linked to a species active
PT against disease
XX
PS Disclosure; Page 4; 30pp; English.
XX
CC AAQ99458 and AAQ99459 are hypoxia inducible transcription control
CC elements P24 and P18, respectively. P24 and P18 may be linked to at
CC least one gene encoding a protein that has activity against disease e.g.
CC CD2,CD4, etc. Such a construct may be used to treat a patient
CC suffering from a disease in which hypoxia is a cause or symptom.
CC The constructs are particularly used for treating tumours.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 90.5%; Score 19; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 21 TGTCACGTCCTGCACGACG 3

RESULT 7
AAZ11422/c
ID AAZ11422 standard; DNA; 24 BP.
XX
AC AAZ11422;
XX
DT 26-OCT-1999 (first entry)
XX
DE Hypoxia responsive sequence mPGK.
XX
KW Retroviral vector; functional splice donor site; hybrid viral vector;
KW functional splice acceptor site; in vivo gene delivery; therapeutic;
KW lentiviral vector; modified hematopoietic stem cell; MHSC; tumour;
KW ischemia; hypoxia response element; HRE; hypoxia; ss.
XX
OS Mus sp.
XX
PN WO9915684-A2.
XX
PD 01-APR-1999.
XX
PF 23-SEP-1998; 98WO-GB02885.
XX
PR 25-SEP-1997; 97GB-0020465.
PR 23-SEP-1997; 97GB-0020216.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Bebbington C, Binley KM, Lewis C, Naylor S;
XX
DR WPI; 1999-263482/22.
XX
PT New retroviral vectors, for, e.g. delivering nucleotide sequences to
PT solid tumor sites
XX
PS Example 1 (page 68); Fig 1 (page 1/43); 288pp; English.
XX
CC The invention relates to a retroviral vector (RVV) comprising a
CC functional splice donor site (FSDS) and a functional splice acceptor
CC site (FSAS) where: (i) the FSDS and the FSAS flank a first nucleotide
CC sequence of interest (NOI); (ii) the FSDS is upstream of the FSAS; (iii)
CC the RVV is derived from a retroviral pro-vector; (iv) the retroviral
CC pro-vector comprises a first nucleotide sequence (NS) capable of yielding
CC the FSDS and a second NS capable of yielding the FSAS; and (v) the first
CC NS is downstream of the second NS, such that the RVV is formed as a
CC result of reverse transcription of the retroviral pro-vector. A hybrid
CC viral vector (VV) system for in vivo gene delivery, which system
CC comprises a primary VV which encodes a secondary VV, the primary vector

CC capable of infecting a first target cell and of expressing the secondary
CC VV, which secondary vector is capable of transducing a secondary target
CC cell, where the primary vector is obtainable from or is based on a
CC adenoviral vector and the secondary VV is obtainable from or is based on
CC a RVV preferably a lentiviral vector (LVV) is also provided. The systems
CC can be used for delivering NOIs to one or more target sites. The NOIs may
CC encode therapeutic or diagnostic agents. The methods are used
CC particularly for producing modified hematopoietic stem cells (MHSCs) to
CC deliver NOIs to sites such as solid tumours which are characterised by
CC ischemia, such as hypoxia or low glucose concentration. The system
CC permits the stable expression of NOIs in targeted cells, e.g. rapidly
CC dividing cells. Sequences AAZ11420-430 represent nucleotide sequences
CC that are esponsive to hypoxia.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 90.5%; Score 19; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 21 TGTCACGTCCTGCACGACG 3

RESULT 8
AAA12007/c
ID AAA12007 standard; DNA; 24 BP.
XX
AC AAA12007;
XX
DT 14-AUG-2000 (first entry)
XX
DE Murine HRE mPGK DNA.
XX
KW HRE; hypoxia response element; hypoxia-inducible factor; HIF; vasotropic;
KW cardiant; cytostatic; antiarthritic; gene therapy; ischaemia; arthritis;
KW cardiovascular disease; peripheral arterial disease; cancer; murine; ds.
XX
OS Mus sp.
XX
PN WO200017371-A1.
XX
PD 30-MAR-2000.
XX
PF 22-SEP-1999; 99WO-GB03181.
XX
PR 23-SEP-1998; 98WO-GB02885.
PR 28-JAN-1999; 99GB-0001906.
PR 16-FEB-1999; 99GB-0003538.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Binley KM, Naylor S;
XX
DR WPI; 2000-283595/24.
XX
PT Novel polynucleotide constructs comprising at least two repeats of a
PT hypoxia response element useful for driving expression of nucleic acids
PT of interest in a cell under hypoxic conditions -
XX
PS Disclosure; Page 11; 155pp; English.
XX
CC This invention describes novel polynucleotide comprising at least 2
CC repeats of a hypoxia response element (HRE), where the hypoxia-inducible
CC factor (HIF) consensus binding sites within each of the 2 repeats are
CC separated by a spacer of at least 20 contiguous nucleotides. The products
CC of the invention have vasotropic, cardiant, cytostatic and antiarthritic
CC activity and can be used for gene therapy. The polynucleotides are useful
CC for delivering nucleic acids of interest to mammalian cells. Lentiviral
CC vectors are responsive to hypoxic agents and to agents that mimic
CC hypoxia. This regulation can be harnessed in vitro to enhance the
CC production of the vector and can be used in vivo to regulate gene
CC expression in response to a physiological signal. The vectors have
CC utility in disease, where ischaemia, including hypoxia, is a feature,
CC e.g. cardiovascular disease, peripheral arterial disease, cancer and
CC arthritis. The novel regulatory construct is capable of driving very high
CC levels of transcription under conditions of hypoxia whilst providing only
CC low basal levels of transcription under normal oxygen conditions. The
CC polynucleotide construct targets cells within a tumor mass that are under
CC conditions of hypoxia without affecting normal surrounding tissue. This
CC sequence represents a murine HRE DNA fragment which is described in the
CC method of the invention.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 90.5%; Score 19; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 21 TGTCACGTCCTGCACGACG 3

RESULT 9
AAC88980/c
ID AAC88980 standard; DNA; 24 BP.
XX
AC AAC88980;
XX
DT 06-MAR-2001 (first entry)
XX
DE Murine hypoxic response element PGK-1 HRE.
XX
KW Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
KW hypoxia inducible factor-1; cancer; ischaemia; ds.
XX
OS Mus sp.
XX
PN WO200069908-A1.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-GB01826.
XX
PR 12-MAY-1999; 99GB-0011047.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Ratcliffe PJ, Maxwell PH, Pugh CW;
XX
DR WPI; 2001-025006/03.
XX
PT Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF)
PT alpha subunit interaction modulators for treating ischemia by
PT contacting a VHL protein and an HIF subunit protein with a putative
PT modulator -
XX
PS Examples; Page 43; 56pp; English.
XX
CC The present invention describes a novel assay for use in identifying
CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
CC contacting the VHL protein, the HIF-1alpha subunit and the putative
CC modulator under conditions where the former two would normally complex.
CC Modulators of this type are useful in the treatment of cancer and
CC ischaemic conditions such as coronary, cerebral and vascular
CC insufficiency.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 90.5%; Score 19; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||
Db         21 TGTCACGTCCTGCACGACG 3
```

RESULT 10
AAH42140
ID AAH42140 standard; DNA; 123 BP.
XX
AC AAH42140;
XX
DT 17-SEP-2001 (first entry)
XX
DE Synapsin gene SIL element and phosphoroglycerate kinase gene HRE element.
XX
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalessemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoroglycerate kinase gene; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200148187-A2.
XX
PD 05-JUL-2001.
XX
PF 15-DEC-2000; 2000WO-US33269.
XX
PR 23-DEC-1999; 99US-0171597.
PR 28-NOV-2000; 2000US-0723326.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Webster KA;
XX
DR WPI; 2001-441715/47.
XX
PT Novel isolated expression vector useful therapeutically, comprisessa
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 25; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalessemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoroglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
SQ Sequence 123 BP; 22 A; 47 C; 32 G; 22 T; 0 other;

Query Match 90.5%; Score 19; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGTCACGTCCTGCACGACG 19
              ||||||||||||||||||
Db        101 TGTCACGTCCTGCACGACG 119
```

RESULT 11
AAZ11398/c
ID AAZ11398 standard; DNA; 229 BP.
XX
AC AAZ11398;
XX
DT 26-OCT-1999 (first entry)
XX
DE PGK derived enhancer sequence in the context of MLV retroviral promoter.
XX
KW Retroviral vector; functional splice donor site; hybrid viral vector;
KW functional splice acceptor site; in vivo gene delivery; therapeutic;
KW lentiviral vector; modified hematopoietic stem cell; MHSC; tumour;
KW ischemia; hypoxia response element; HRE; hypoxia; ss.
XX
OS Synthetic.
OS Mus sp.
OS Murine leukemia virus.
XX
PN WO9915684-A2.
XX
PD 01-APR-1999.
XX
PF 23-SEP-1998; 98WO-GB02885.
XX
PR 25-SEP-1997; 97GB-0020465.
PR 23-SEP-1997; 97GB-0020216.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Bebbington C, Binley KM, Lewis C, Naylor S;
XX
DR WPI; 1999-263482/22.
XX
PT New retroviral vectors, for, e.g. delivering nucleotide sequences to
PT solid tumor sites
XX
PS Example 1; Page 70; 288pp; English.
XX
CC The invention relates to a retroviral vector (RVV) comprising a
CC functional splice donor site (FSDS) and a functional splice acceptor site
CC (FSAS) where: (i) the FSDS and the FSAS flank a first nucleotide sequence
CC of interest (NOI); (ii) the FSDS is upstream of the FSAS; (iii) the RVV
CC is derived from a retroviral pro-vector; (iv) the retroviral pro-vector
CC comprises a first nucleotide sequence (NS) capable of yielding the FSDS
CC and a second NS capable of yielding the FSAS; and (v) the first NS is
CC downstream of the second NS, such that the RVV is formed as a result of
CC reverse transcription of the retroviral pro-vector. A hybrid viral vector
CC (VV) system for in vivo gene delivery, which system comprises a primary
CC VV which encodes a secondary VV, the primary vector capable of infecting
CC a first target cell and of expressing the secondary VV, which secondary
CC vector is capable of transducing a secondary target cell, where the
CC primary vector is obtainable from or is based on a adenoviral vector and
CC the secondary VV is obtainable from or is based on a RVV preferably a
CC lentiviral vector (LVV) is also provided. The systems can be used for
CC delivering NOIs to one or more target sites. The NOIs may encode
CC therapeutic or diagnostic agents. The methods are used particularly for
CC producing modified hematopoietic stem cells (MHSCs) to deliver NOIs to
CC sites such as solid tumours which are characterised by ischemia, such as
CC hypoxia or low glucose concentration. The system permits the stable
CC expression of NOIs in targeted cells, e.g. rapidly dividing cells. The
CC present sequence represents a PGK derived enhancer sequence in the
CC context of MLV retroviral promoter, in the forward orientation.
XX

SQ Sequence 229 BP; 52 A; 68 C; 55 G; 54 T; 0 other;

Query Match 90.5%; Score 19; DB 20; Length 229;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 30 TGTCACGTCCTGCACGACG 12

RESULT 12
AAA11996/c
ID AAA11996 standard; DNA; 229 BP.
XX
AC AAA11996;

14-AUG-2000 (first entry)

DE Murine PGK HRE derived enhancer DNA.
XX
KW HRE; hypoxia response element; hypoxia-inducible factor; HIF; vasotropic;
KW cardiant; cytostatic; antiarthritic; gene therapy; ischaemia; arthritis;
KW cardiovascular disease; peripheral arterial disease; cancer;
KW phosphoglycerate kinase; PGK; murine; enhancer; ds.
XX
OS Mus sp.
XX
PN WO200017371-A1.
XX
PD 30-MAR-2000.
XX
PF 22-SEP-1999; 99WO-GB03181.
XX
PR 23-SEP-1998; 98WO-GB02885.
PR 28-JAN-1999; 99GB-0001906.
PR 16-FEB-1999; 99GB-0003538.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Binley KM, Naylor S;
XX
DR WPI; 2000-283595/24.
XX
PT Novel polynucleotide constructs comprising at least two repeats of a
PT hypoxia response element useful for driving expression of nucleic acids
PT of interest in a cell under hypoxic conditions -
XX
PS Example 3; Page 74-75; 155pp; English.
XX
CC This invention describes novel polynucleotide comprising at least 2
CC repeats of a hypoxia response element (HRE), where the hypoxia-inducible
CC factor (HIF) consensus binding sites within each of the 2 repeats are
CC separated by a spacer of at least 20 contiguous nucleotides. The products
CC of the invention have vasotropic, cardiant, cytostatic and antiarthritic
CC activity and can be used for gene therapy. The polynucleotides are useful
CC for delivering nucleic acids of interest to mammalian cells. Lentiviral
CC vectors are responsive to hypoxic agents and to agents that mimic
CC hypoxia. This regulation can be harnessed in vitro to enhance the
CC production of the vector and can be used in vivo to regulate gene
CC expression in response to a physiological signal. The vectors have
CC utility in disease, where ischaemia, including hypoxia, is a feature,
CC e.g. cardiovascular disease, peripheral arterial disease, cancer and
CC arthritis. The novel regulatory construct is capable of driving very high
CC levels of transcription under conditions of hypoxia whilst providing only
CC low basal levels of transcription under normal oxygen conditions. The
CC polynucleotide construct targets cells within a tumor mass that are under
CC conditions of hypoxia without affecting normal surrounding tissue. This
CC sequence represents a murine phosphoglycerate kinase (PGK) HRE derived
CC enhancer which is described in the method of the invention.
XX
SQ Sequence 229 BP; 52 A; 68 C; 55 G; 54 T; 0 other;

Query Match 90.5%; Score 19; DB 21; Length 229;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 30 TGTCACGTCCTGCACGACG 12

RESULT 13
AAH20729/c
ID AAH20729 standard; DNA; 513 BP.
XX
AC AAH20729;
XX
DT 13-AUG-2001 (first entry)
XX
DE Murine phosphoglycerate kinase promoter DNA.
XX
KW Phosphoglycerate kinase; promoter; gene therapy; amniocyte; cytostatic;
KW E1A region; E1B region; modified tropism; tumor; ds.
XX
OS Mus sp.
XX
PN WO200136615-A2.
XX
PD 25-MAY-2001.
XX
PF 07-NOV-2000; 2000WO-EP10992.
XX
PR 18-NOV-1999; 99DE-1055558.
XX
PA (KOCH/) KOCHANEK S.
XX
PI Kochanek S, Schiedner G;
XX
DR WPI; 2001-343817/36.
XX
PT New permanent amniocyte cell lines, useful for producing viral gene
PT therapy vectors or mutant adenoviruses, express the adenoviral E1A and
PT E1B gene products -
XX
PS Example 1; Page 61; 72pp; German.
XX
CC This invention describes novel permanent amniocyte cell lines (A),
CC containing at least one nucleic acid (I) that causes expression of the
CC gene products (II) of the adenoviral E1A and E1B regions. (A) are used to
CC produce gene therapy vectors, especially adeno, adeno-associated, retro
CC or lenti viral vectors, particularly first- or second generation,
CC large-capacity or deleted adenoviral vectors. (A) are also used to
CC produce adenoviral mutants, optionally with modified tropism. The vectors
CC may express a wide range of therapeutic proteins or antisense RNAs.
CC Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
CC for treating tumors, they replicate in the cells but not significantly in
CC normal primary cells. (A) can be made efficiently, simply and
CC reproducibly. The products of the invention have cytostatic activity.
CC This sequence represents the murine phosphoglycerate kinase promoter
CC found in plasmid STK146.
XX
SQ Sequence 513 BP; 79 A; 171 C; 161 G; 102 T; 0 other;

Query Match 90.5%; Score 19; DB 22; Length 513;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 235 TGTCACGTCCTGCACGACG 217

RESULT 14
AAS05243/c
ID AAS05243 standard; DNA; 4768 BP.

XX
AC AAS05243;
XX
DT 07-SEP-2001 (first entry)
XX
DE Plasmid vector pDG2 used as a construct for TRP genes.
XX
KW Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; pDG2;
KW transgenic animal; knockout mouse; triplet repeat expansion;
KW fragile X syndrome; Huntington's disease; cyclic; circular; ds.
XX
OS Synthetic.
XX
PN WO200130798-A1.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29382.
XX
PR 26-OCT-1999; 99US-0161488.
XX
PA (DELT-) DELTAGEN INC.

Klein R, Matthews W, Moore M, Allen KD;

DR WPI; 2001-300473/31.
XX
PT Novel transgenic animals useful as animal model for characterization of
PT function of a gene encoding trinucleotide repeat proteins (TRPs),
PT contains heterozygous disruption in a gene encoding TRP -
XX
PS Disclosure; Fig 2B; 106pp; English.
XX
CC The present sequence for plasmid vector pDG2 is used as a construct
CC for genes encoding trinucleotide repeat proteins (TRP) such as gene
CC T243 to produce disruption in the DNA. The invention describes
CC methods of producing embryonic stem (ES) cells comprising a heterozygous
CC disruption in a target DNA sequence (preferably T243) encoding a TRP and
CC of producing a knockout mouse comprising a homozygous disruption in a
CC gene encoding TRP, where the disruption inhibits the production of the
CC wild type TRP. The invention also relates to identifying agents capable
CC of affecting a phenotype of a knockout mouse. Also described are methods
CC of determining whether expansion of the trinucleotide repeat in a gene
CC encoding TRP produces a phenotypic change. The transgenic animals and
CC the cells are useful for identifying compounds capable of ameliorating
CC disease symptoms, and as test substrates for the identification of drugs,
CC pharmaceuticals, therapies and interventions which may be effective in
CC treating trinucleotide repeat disorders e.g. fragile X syndrome and
CC Huntington's disease. The animal models for trinucleotide repeat
CC disorders are ideal model systems to study the progression of disease in
CC vivo, the molecular basis of these diseases and show the features
CC observed in human disease. Using the mice, it is possible to model both
CC the pathogenic mechanism and the trinucleotide repeat instability in the
CC mouse.
XX
SQ Sequence 4768 BP; 1124 A; 1218 C; 1269 G; 1157 T; 0 other;

Query Match 90.5%; Score 19; DB 22; Length 4768;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 2838 TGTCACGTCCTGCACGACG 2820

RESULT 15
ABL42019/c
ID ABL42019 standard; DNA; 4768 BP.
XX
AC ABL42019;
XX
DT 11-JUN-2002 (first entry)
XX
DE Nucleotide sequence of vector pDG2.
XX
KW pDG2; transgenic animal; matrix metalloproteinase-23 gene; MMP-23 gene;
KW ss.
XX
OS Synthetic.
XX
PN US2002023275-A1.
XX
PD 21-FEB-2002.
XX
PF 17-MAY-2001; 2001US-0861077.
XX
PR 17-MAY-2000; 2000US-204972P.
PR 29-JUN-2000; 2000US-215394P.
XX
PA (LEVI/) LEVITEN M W.
XX
PI Leviten MW;
XX
DR WPI; 2002-255684/30.
XX
PT Non-human transgenic animal useful as a model for disease and for
PT identifying agents that modulate gene expression and gene function,
PT comprises a disruption in the matrix metalloproteinase-23 gene -
XX
PS Example 1; Fig 2B; 38pp; English.
XX
CC The present sequence represents vector pDG2. This vector contains an
CC ampicillin resistance gene and a neomycin gene. The vector is used in
CC the invention. The specification describes a non-human transgenic animal
CC comprising a disruption in the matrix metalloproteinase (MMP)-23 gene.
CC Transgenic animals of the invention comprising a homozygous or
CC heterozygous disruption in MMP23 gene are useful for identifying agents
CC which modulate MMP23 expression or function. They are also useful for
CC identifying agents that are capable of ameliorating a phenotype of a
CC transgenic animal comprising a disruption in an MMP-23 gene or
CC ameliorating a disease associated with the phenotype of a transgenic
CC animal comprising a disruption in the MMP-23 gene. The animals are
CC useful as an animal model for diseases, disorders and conditions
CC characterized by a disruption in a gene encoding a metalloproteinase,
CC more particularly disease, disorders and conditions associated with the
CC phenotypes demonstrated by the knockout mice. The transgenic animals
CC are useful as test substrates for identification of drugs,
CC pharmaceuticals and therapies effective in treating diseases, disorders
CC and conditions associated with disruption in the target gene. The
CC animal is useful for testing and developing new treatments relating
CC to behavioural phenotypes demonstrated by the animal models.
XX
SQ Sequence 4768 BP; 1124 A; 1218 C; 1269 G; 1157 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 4768;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACG 19
||||||||||||||||||||
Db 2838 TGTCACGTCCTGCACGACG 2820

Search completed: July 9, 2003, 14:21:43
Job time : 147 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:55 ; Search time 1136 Seconds
(without alignments)
299.388 Million cell updates/sec

Title: US-09-723-326B-1
Perfect score: 21
Sequence: 1 tgtcacgtcctgcacgacgta 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	81.0	553	17	BH887440	BH887440 LB01441a.
c	2	17	81.0	631	17	BH888010	BH888010 LB01794a.
	3	16.8	80.0	395	12	BG286598	BG286598 602381606
	4	16.8	80.0	594	14	BQ664135	BQ664135 HV02A03u
	5	16.8	80.0	927	10	BE290997	BE290997 601084169
	6	16.8	80.0	1098	17	CNS06T4V	AL414101 T7 end of
c	7	16.8	80.0	1574	17	AZ133021	AZ133021 OSJNBb010
c	8	16.4	78.1	307	17	AZ578287	AZ578287 21b03 Sho
c	9	16.4	78.1	383	12	BF743507	BF743507 QV0-BT084
	10	16.4	78.1	419	13	BM322991	BM322991 PIC1_11_B
	11	16.4	78.1	615	17	AQ397741	AQ397741 mgxb0017I
c	12	16.2	77.1	197	17	BH049064	BH049064 RPCI-24-2
c	13	16.2	77.1	343	12	BE836447	BE836447 PM2-FN006
	14	16.2	77.1	544	17	AQ078346	AQ078346 CIT-HSP-2
	15	16.2	77.1	622	17	BH141668	BH141668 TDGDG37TH
c	16	16.2	77.1	661	17	AG136658	AG136658 Pan trogl
	17	16.2	77.1	690	13	BI151875	BI151875 602916373
	18	16.2	77.1	920	17	CNS029RJ	AL187624 Tetraodon
	19	16.2	77.1	930	17	CNS04EK8	AL287153 Tetraodon
c	20	16.2	77.1	1123	14	BQ712663	BQ712663 AGENCOURT
	21	16.2	77.1	1126	17	CNS03KVB	AL248672 Tetraodon
c	22	16.2	77.1	1655	12	BG483774	BG483774 602503419
c	23	16.2	77.1	1874	10	AW729726	AW729726 GA__Ea002
	24	16	76.2	404	17	AQ113596	AQ113596 CIT-HSP-2
	25	15.8	75.2	186	12	BG188939	BG188939 RST7974 A
c	26	15.8	75.2	197	12	BG190578	BG190578 RST9651 A
c	27	15.8	75.2	199	12	BG197706	BG197706 RST16935
	28	15.8	75.2	219	12	BG185274	BG185274 RST4213 A
	29	15.8	75.2	220	12	BG212794	BG212794 RST32389
	30	15.8	75.2	221	12	BG192598	BG192598 RST11713
	31	15.8	75.2	226	12	BG190058	BG190058 RST9114 A
	32	15.8	75.2	231	12	BG198722	BG198722 RST17991
	33	15.8	75.2	236	12	BG203387	BG203387 RST22768
c	34	15.8	75.2	288	14	BM965404	BM965404 kj95d12.y
	35	15.8	75.2	431	17	BH753428	BH753428 SALK_0288
c	36	15.8	75.2	454	10	AV619431	AV619431 AV619431
	37	15.8	75.2	466	9	AJ280880	AJ280880 4A3A-AAY-
	38	15.8	75.2	467	9	AL587460	AL587460 AL587460
c	39	15.8	75.2	482	12	BF625474	BF625474 HVSMEa000
c	40	15.8	75.2	498	10	AW592678	AW592678 hf46a04.x
c	41	15.8	75.2	520	13	BI776024	BI776024 468768 MA
c	42	15.8	75.2	571	17	L1091AY	AL354057 Leishmani
c	43	15.8	75.2	588	14	BU005199	BU005199 QGG7G14.y
	44	15.8	75.2	604	13	BM340142	BM340142 MEST319-A
c	45	15.8	75.2	608	14	BQ483290	BQ483290 WHE3506_G

ALIGNMENTS

RESULT 1
BH887440/c
LOCUS BH887440 553 bp DNA linear GSS 07-AUG-2002
DEFINITION LB01441a.d_SP6.1 Leishmania major Friedlin BAC Library Leishmania major genomic clone LB01441a, DNA sequence.
ACCESSION BH887440
VERSION BH887440.1 GI:22132375
KEYWORDS GSS.
SOURCE Leishmania major.
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
REFERENCE 1 (bases 1 to 553)
AUTHORS Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E., Stuart,K. and Ragland,M.
TITLE Leishmania major Friedlin BAC End Sequences
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: LB01441a.d_T7.1
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seatttle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: SP6
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .553

/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="LB01441a"
/clone_lib="Leishmania major Friedlin BAC Library"
/lab_host="E. coli GeneHogs + TrfA"
/note="Vector: pCG270; Site_1: HindIII; Genomic DNA from Leishmania major Friedlin in agarose blocks was partially digested with HindIII, size selected, and ligated with HindIII-digested pCG270 vector DNA. 10368 clones were picked and arrayed in 384- and 96-will plates. Library construction and arraying was carried out by ResGen Corporation and clones and filters are available from them"

BASE COUNT 89 a 175 c 191 g 98 t
ORIGIN

Query Match 81.0%; Score 17; DB 17; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACGTCCTGCACGACGT 20
||||||||||||||||
Db 427 CACGTCCTGCACGACGT 411

RESULT 2
BH888010/c
LOCUS BH888010 631 bp DNA linear GSS 07-AUG-2002
DEFINITION LB01794a.d_T7.1 Leishmania major Friedlin BAC Library Leishmania major genomic clone LB01794a, DNA sequence.
ACCESSION BH888010
VERSION BH888010.1 GI:22133715
KEYWORDS GSS.
SOURCE Leishmania major.
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
REFERENCE 1 (bases 1 to 631)
AUTHORS Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E., Stuart,K. and Ragland,M.
TITLE Leishmania major Friedlin BAC End Sequences
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: LB01794a.d_SP6.1
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seatttle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .631
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="LB01794a"
/clone_lib="Leishmania major Friedlin BAC Library"
/lab_host="E. coli GeneHogs + TrfA"
/note="Vector: pCG270; Site_1: HindIII; Genomic DNA from Leishmania major Friedlin in agarose blocks was partially digested with HindIII, size selected, and ligated with HindIII-digested pCG270 vector DNA. 10368 clones were picked and arrayed in 384- and 96-will plates. Library construction and arraying was carried out by ResGen Corporation and clones and filters are available from them"

BASE COUNT 104 a 189 c 224 g 114 t
ORIGIN

Query Match 81.0%; Score 17; DB 17; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACGTCCTGCACGACGT 20
||||||||||||||||
Db 428 CACGTCCTGCACGACGT 412

RESULT 3
BG286598
LOCUS BG286598 395 bp mRNA linear EST 21-FEB-2001
DEFINITION 602381606F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4499448 5', mRNA sequence.
ACCESSION BG286598
VERSION BG286598.1 GI:13039617
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10363 row: k column: 01
High quality sequence stop: 388.
FEATURES Location/Qualifiers
source 1. .395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4499448"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 85 a 97 c 117 g 96 t
ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 395;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACGTCCTGCACGACGTA 21
|||||||| ||||||| |||
Db 248 GTCACGTCGTGCACGAGGTA 267

RESULT 4
BQ664135
LOCUS BQ664135 594 bp mRNA linear EST 15-JUL-2002
DEFINITION HV02A03u HV Hordeum vulgare cDNA clone HV02A03 3-PRIME, mRNA sequence.
ACCESSION BQ664135
VERSION BQ664135.1 GI:21805268
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

```
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and Graner
            ,A.
  TITLE     Barley ESTs from germinating seeds
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Stein Nils
            Molecular Markers Group, Department Genbank
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Corrensstr. 3, 06466, Gatersleben, Germany
            Tel: 039482-5522
            Fax: 039482-5595
            Email: stein@ipk-gatersleben.de
            Insert Length: 594   Std Error: 0.00
            Plate: 2  row: A  column: 3
            Seq primer: M13uni.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Hordeum vulgare"
                     /cultivar="Barke"
                     /db_xref="GABI:147814"
                     /db_xref="taxon:4513"
                     /clone="HV02A03"
                     /clone_lib="HV"
                     /tissue_type="germinating seeds"
                     /dev_stage="germinating seeds (48-96 h)"
                     /lab_host="XL10-Gold"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
                     cDNA); Site_2: XhoI (3'-end of cDNA); Roots were grown for
                     two days on filter paper at room temperature. Due to a
                     cloning artefact caused by the kit, in most cases the
                     EcoRI site is NOT present, as well as the EcoRIadapter
                     used for cloning. To excise the insert, restriction sites
                     upstream EcoRI should be used (e.g. BamHI, SalI,PstI).
                     NOTE: Also due to the cloning system used Blue/white
                     selection for recombinats is not 100% reliable.Average
                     insert size is 1 kb"
BASE COUNT       89 a    242 c    172 g     91 t
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 14;  Length 594;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACGT 20
              ||| |||||| |||||||||
          284 TGTGACGTCCGGCACGACGT 303


RESULT 5
BE290997
LOCUS       BE290997                927 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  601084169F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3498353 5',
            mRNA sequence.
ACCESSION   BE290997
VERSION     BE290997.1  GI:9172417
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8553  row: j  column: 18
            High quality sequence start: 3
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .927
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3498353"
                     /clone_lib="NCI_CGAP_Mam6"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      355 a    183 c    253 g    136 t
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 10;  Length 927;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACGT 20
              ||||||||| |||||| |||
Db         18 TGTCACGTCGTGCACGCCGT 37


RESULT 6
CNS06T4V
LOCUS       CNS06T4V                1098 bp    DNA     linear   GSS 05-JUL-2001
DEFINITION  T7 end of clone AW0AA028H07 of library AW0AA from strain CLIB 89 of
            Yarrowia lipolytica, genomic survey sequence.
ACCESSION   AL414101
VERSION     AL414101.1  GI:12186881
KEYWORDS    GSS.
SOURCE      Yarrowia lipolytica.
  ORGANISM  Yarrowia lipolytica
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Dipodascaceae; Yarrowia.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 1098)
  AUTHORS   Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynerol,C.,
            Artiguenave,F., Wincker,P. and Gaillardin,C.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
            lipolytica
  JOURNAL   FEBS Lett. 487 (1), 95-100 (2000)
  MEDLINE   20584727
   PUBMED   11152892
REFERENCE   3  (bases 1 to 1098)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
```

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

```
FEATURES             Location/Qualifiers
     source          1. .1098
                     /organism="Yarrowia lipolytica"
                     /strain="CLIB 89"
                     /db_xref="taxon:4952"
                     /clone="AW0AA028H07"
                     /clone_lib="AW0AA"
                     /note="end : T7"
BASE COUNT      279 a    290 c    257 g    268 t      4 others
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 17;  Length 1098;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACGT 20
              |||||||||| ||||| |||
          913 TGTCACGTCCAGCACGCCGT 932


RESULT 7
AZ133021/c
LOCUS       AZ133021               1574 bp    DNA     linear   GSS 02-JUN-2000
DEFINITION  OSJNBb0108I24f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic
            clone OSJNBb0108I24f, DNA sequence.
ACCESSION   AZ133021
VERSION     AZ133021.1  GI:8211768
KEYWORDS    GSS.
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 1574)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: GTAAAACGACGGCCAGTG
            Class: BAC ends
            High quality sequence stop: 1574.
FEATURES             Location/Qualifiers
     source          1. .1574
                     /organism="Oryza sativa"
                     /strain="Japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:4530"
                     /clone="OSJNBb0108I24f"
                     /clone_lib="CUGI Rice BAC Library (EcoRI)"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                     Rice is the most important food crop in the world. Half of
                     the world population, especially those inhabiting highly
                     populated areas of the humid tropics and subtropics, rely
                     on rice as their primary source of carbohydrate.
                     Monocotyledonous rice is a diploid plant (2n=24) with a
                     haploid genome equivalent of 431 Mbp (Arumuganathan and
                     Earle, 1991). The relatively small genome of rice, three
                     times larger than that of Arabidopsis, makes it suitable
                     for genomic studies. In order to facilitate positional
                     cloning, physical mapping and genome sequencing of rice,
                     we have constructed a BAC library from Oryza sativa,
                     Nipponbare variety using EcoRI as the cloning enzyme. The
                     library contains 55,296 clones with an average insert size
                     of 121 Kb providing approximatley 15 haploid genome
                     equivalents. The deep coverage allows the isolation a
                     particular sequence with a probability of 99.9 %. Three
                     high density filters, each containing 18,432 clones
                     (doubly spotted), represent the whole library for colony
                     screening and can be requested from the Clemson University
                     BAC/EST Resource Center (www.genome.clemson.edu)."
BASE COUNT      381 a    399 c    323 g    466 t      5 others
ORIGIN

  Query Match             80.0%;  Score 16.8;  DB 17;  Length 1574;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTCACGTCCTGCACGACGTA 21
              |||||||||||| || ||||
Db        739 GTCACGTCCTGCGCGCCGTA 720


RESULT 8
AZ578287/c
LOCUS       AZ578287               307 bp    DNA     linear   GSS 08-DEC-2000
DEFINITION  21b03 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
            sp. NGR234 genomic clone 21b03, DNA sequence.
ACCESSION   AZ578287
VERSION     AZ578287.1  GI:11605415
KEYWORDS    GSS.
SOURCE      Rhizobium sp. NGR234.
  ORGANISM  Rhizobium sp. NGR234
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Rhizobium.
REFERENCE   1  (bases 1 to 307)
  AUTHORS   Viprey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
  TITLE     Genetic snapshots of the Rhizobium species NGR234 genome
  JOURNAL   Genome Biol. 1 (6), RESEARCH0014 (2000)
  MEDLINE   21114532
COMMENT     Contact: Virginie.Viprey
            Laboratoire de Biologie Moleculaire des Plantes Superieures
            University of Geneva
            1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
            Tel: +44(0)1603450000
            Fax: +44(0)1603450045
            Email: virginie.viprey@bbsrc.ac.uk
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .307
                     /organism="Rhizobium sp. NGR234"
                     /strain="ANU265"
                     /db_xref="taxon:394"
                     /clone="21b03"
                     /clone_lib="Shot-gun genomic library of Rhizobium strain
                     ANU265"
                     /note="Vector: M13; derivative strain of NGR234 cured of
                     pNGR234a"
BASE COUNT       64 a     93 c     90 g     60 t
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 17;  Length 307;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCACGTCCTGCACGACGT 20
              | ||||||||||||||||
Db        199 TGACGTCCTGCACGACGT 182


RESULT 9
BF743507/c
LOCUS       BF743507               383 bp    mRNA    linear   EST 10-JAN-2001
DEFINITION  QV0-BT0846-121000-434-e09 BT0846 Homo sapiens cDNA, mRNA sequence.
```

```
ACCESSION   BF743507
VERSION     BF743507.1  GI:12070183
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
  COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV0&t2=QV0-BT0846-
            121000-434-e09&t3=2000-10-12&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 10
            High quality sequence stop: 97.
FEATURES             Location/Qualifiers
     source          1. .383
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT0846"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      100 a     91 c    100 g     92 t
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 12;  Length 383;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CACGTCCTGCACGACGTA 21
              | ||||||||||||||||
Db         22 CCCGTCCTGCACGACGTA 5


RESULT 10
BM322991
LOCUS       BM322991                419 bp    mRNA    linear   EST 04-JAN-2002
DEFINITION  PIC1_11_B07.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
            bicolor cDNA, mRNA sequence.
ACCESSION   BM322991
VERSION     BM322991.1  GI:18060397
KEYWORDS    EST.
SOURCE      sorghum.
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
            Sudman,M. and Pratt,L.H.
  TITLE     An EST database from Sorghum: plants infected with a compatible
            pathogen
  JOURNAL   Unpublished (2002)
  COMMENT   Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20. Three-prime sequences, which are obtained with PolyTMix or
            T7 sequencing primer, are presented as the reverse complement.
            Seq primer: JEN REV
            High quality sequence stop: 413
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Sorghum bicolor"
                     /cultivar="BTx623"
                     /db_xref="taxon:4558"
                     /clone_lib="Pathogen-infected compatible 1 (PIC1)"
                     /tissue_type="Leaves"
                     /dev_stage="4-week-old seedlings infected with
                     Colletotrichum graminicola"
                     /note="Vector: pBluescript II SK(-) from Lambda Zap II;
                     Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
                     seedlings were sprayed with spore suspension prepared from
                     3-week-old FRM42I, a sorghum isolate of the anthracnose
                     pathogen Colletotrichum graminicola. Inoculated plants
                     were kept in a 25 C dark growth chamber with 100% relative
                     humidity for 24 hr, followed by 12/12 hr of light/dark
                     cycle at 25 C with 90% relative humidity for another 24
                     hr. All leaves were harvested and quick frozen with liquid
                     nitrogen and stored in a -80 C freezer. The library was
                     made from poly-A RNA in the cloning vector lambda ZAP II.
                     Clones to be sequenced were prepared by mass excision.
                     WARNING: While most or all ESTs are expected to derive
                     from the host plant, no effort was made to eliminate ESTs
                     deriving from the pathogen."
BASE COUNT       73 a    146 c    110 g     90 t
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 13;  Length 419;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GTCACGTCCTGCACGACG 19
              ||||||||||||||| |||
Db        237 GTCACGTCCTGCACCACG 254


RESULT 11
AQ397741
LOCUS       AQ397741                615 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  mgxb0017I11f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
            clone mgxb0017I11f, DNA sequence.
ACCESSION   AQ397741
VERSION     AQ397741.1  GI:4368768
KEYWORDS    GSS.
SOURCE      Magnaporthe grisea.
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
            Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
            Genome
  JOURNAL   Unpublished (1998)
  COMMENT   Contact: Dean RA
```

```
          Clemson University Genomics Institute
          Clemson University
          100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
          Tel: 864 656 5737
          Fax: 864 656 4293
          Email: rdean@clemson.edu
          Seq primer: TAATACGACTCACTATAGGG
          Class: BAC ends
          High quality sequence stop: 216.
FEATURES             Location/Qualifiers
     source          1. .615
                     /organism="Magnaporthe grisea"
                     /strain="70-15"
                     /db_xref="taxon:148305"
                     /clone="mgxb0017I11f"
                     /clone_lib="CUGI Rice Blast BAC Library"
                     /tissue_type="Protoplasts"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
                     Rice blast is one of the most devestating fungal diseases
                     of rice world wide. It is a filamentous ascomycete with
                     a haploid genome (n=7) of approximately 40 Mbp. Rice
                     blast is an important model fungal pathogen for studying
                     numerous aspects of the fungal-host interaction. In
                     order to facilitate genome wide analysis, a BAC library
                     containing 9216 clones with an average insert size of 130
                     kbp was constructed. This library represents greater
                     than 25X genome coverage. High density colony filters
                     are available upon request."
BASE COUNT       97 a    244 c    140 g    134 t
ORIGIN

  Query Match             78.1%;  Score 16.4;  DB 17;  Length 615;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGAC 18
              ||||||||||| ||||||
Db        332 TGTCACGTCCTCCACGAC 349


RESULT 12
BH049064/c
LOCUS       BH049064                197 bp    DNA     linear   GSS 17-JUL-2001
DEFINITION  RPCI-24-232K18.TJ RPCI-24 Mus musculus genomic clone RPCI-24-232K18
            , DNA sequence.
ACCESSION   BH049064
VERSION     BH049064.1  GI:14837619
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 232  row: K  column: 18
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-232K18"
                     /clone_lib="RPCI-24"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI partially digested male C57BL/6J
                     DNA."
BASE COUNT       70 a     32 c     56 g     39 t
ORIGIN

  Query Match             77.1%;  Score 16.2;  DB 17;  Length 197;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGTCACGTCCTGCACGACGTA 21
              ||||| |||||||||| | |||
Db        146 TGTCATGTCCTGCACAAGGTA 126


RESULT 13
BE836447/c
LOCUS       BE836447                343 bp    mRNA    linear   EST 22-SEP-2000
DEFINITION  PM2-FN0061-280600-002-b03 FN0061 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE836447
VERSION     BE836447.1  GI:10268825
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 343)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM2-FN0061-280
            600-002-b03&t3=2000-06-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 57
            High quality sequence stop: 342.
FEATURES             Location/Qualifiers
     source          1. .343
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="FN0061"
                     /dev_stage="Adult"
                     /note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
                     ; Site_2: SmaI; A mini-library was made by cloning
                     products derived from ORESTES PCR (U.S. Letters Patent
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application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 104 a 73 c 87 g 79 t
ORIGIN

Query Match 77.1%; Score 16.2; DB 12; Length 343;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||| ||| ||||||
Db 195 TGTCACGTCTTGCCTGACGTA 175

RESULT 14
AQ078346
LOCUS AQ078346 544 bp DNA linear GSS 20-AUG-1998
DEFINITION CIT-HSP-2363K18.TF CIT-HSP Homo sapiens genomic clone 2363K18, DNA sequence.
ACCESSION AQ078346
VERSION AQ078346.1 GI:3439530
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2363K18.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2363K18"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT 155 a 107 c 123 g 159 t
ORIGIN

Query Match 77.1%; Score 16.2; DB 17; Length 544;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||||| || || |||
Db 434 TGTCACGTCCTTCAGGAGGTA 454

RESULT 15
BH141668
LOCUS BH141668 622 bp DNA linear GSS 16-AUG-2001
DEFINITION TDGDG37TH cTOG Lycopersicon esculentum genomic clone cTOG22G1, DNA sequence.
ACCESSION BH141668
VERSION BH141668.1 GI:15193897
KEYWORDS GSS.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 622)
AUTHORS van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and Tanksley,S.
TITLE Tomato Demethylated Genomic DNA Sequences
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .622
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cTOG22G1"
/clone_lib="cTOG"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb."
BASE COUNT 154 a 170 c 127 g 171 t
ORIGIN

Query Match 77.1%; Score 16.2; DB 17; Length 622;
Best Local Similarity 85.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACGTCCTGCACGACGTA 21
||||||||| ||||| | |||
Db 409 TGTCACGTCTTGCACAAAGTA 429

Search completed: July 9, 2003, 14:40:54
Job time : 1141 secs